

SEQUENCE LISTING

<110> Merck & Co., Inc.

<120> DNA MOLECULES ENCODING HG51, A
G PROTEIN-COUPLED RECEPTOR

<130> 20351 PCT

<150> 60/109,717

<151> 1998-11-24

<160> 15

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1537

<212> DNA

<213> Homo sapien (human)

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ctgagcgcc	ccgcccgcga	ggcgcgcggt	cgccggggcc	tgtactcggg	gaaccgcagc	180
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gggacactga	gccccgcgcc	cctcttcagc	cccggcacct	acgagcgcc	ggcgctgctg	300
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aagttccagc	ggctccgcac	tcccactcac	ctcctcctgg	tcaacatcag	cctcagcgac	420
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tccattgcca	ccctaaccgt	gctggcctat	gaacgttaca	ttcgcggtgt	ccatgccaga	600
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tgcactgtgg	actggaaatc	caaggatgcc	aacgattcct	cctttgtgct	tttcttattt	780
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aaatatgaaa	agaaactggc	caaaatgtgc	tttttaatat	tattcacctt	cctgggtcgt	960
tggatgcctt	atatcgatgt	ctgcttcctg	gtgggttaatg	gtcatggtca	cctgggtcact	1020
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gcaacgaaag	atggggcctt	aaattggatg	ccacttttgg	actttcatca	taagaagtgt	1440
ctggaatacc	cgttctatgt	aatatcaaca	gaaccttgtg	gtccagcagg	aaatccgaat	1500
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<210> 2

<211> 402

<212> PRT

<213> Homo sapien (human)

<400> 2

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Ala	Pro	Leu	Phe	Ser	Pro	Gly	Thr	Tyr	Glu	Arg	Leu	Ala	Leu	Leu	Leu
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Gly	Ser	Ile	Gly	Leu	Leu	Gly	Val	Gly	Asn	Asn	Leu	Leu	Val	Leu	Val
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Leu	Tyr	Tyr	Lys	Phe	Gln	Arg	Leu	Arg	Thr	Pro	Thr	His	Leu	Leu	Leu
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Ile	Ala	Thr	Leu	Thr	Val	Leu	Ala	Tyr	Glu	Arg	Tyr	Ile	Arg	Val	Val
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His	Ala	Arg	Val	Ile	Asn	Phe	Ser	Trp	Ala	Trp	Arg	Ala	Ile	Thr	Tyr
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Ile	Trp	Leu	Tyr	Ser	Leu	Ala	Trp	Ala	Gly	Ala	Pro	Leu	Leu	Gly	Trp
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Asn	Arg	Tyr	Ile	Leu	Asp	Val	His	Gly	Leu	Gly	Cys	Thr	Val	Asp	Trp
			180					185					190		
Lys	Ser	Lys	Asp	Ala	Asn	Asp	Ser	Ser	Phe	Val	Leu	Phe	Leu	Phe	Leu
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Gly	Cys	Leu	Val	Val	Pro	Leu	Gly	Val	Ile	Ala	His	Cys	Tyr	Gly	His
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225					230					235					240
Ile	Gln	Val	Ile	Lys	Ile	Leu	Lys	Tyr	Glu	Lys	Lys	Leu	Ala	Lys	Met
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Cys	Phe	Leu	Met	Ile	Phe	Thr	Phe	Leu	Val	Cys	Trp	Met	Pro	Tyr	Ile
		260						265					270		
Val	Ile	Cys	Phe	Leu	Val	Val	Asn	Gly	His	Gly	His	Leu	Val	Thr	Pro
		275					280					285			
Thr	Ile	Ser	Ile	Val	Ser	Tyr	Leu	Phe	Ala	Lys	Ser	Asn	Thr	Val	Tyr
	290					295					300				
Asn	Pro	Val	Ile	Tyr	Val	Phe	Met	Ile	Arg	Lys	Phe	Arg	Arg	Ser	Leu
305					310					315					320
Leu	Gln	Leu	Leu	Cys	Leu	Arg	Leu	Leu	Arg	Cys	Gln	Arg	Pro	Ala	Lys
			325						330					335	
Asp	Leu	Pro	Ala	Ala	Gly	Ser	Glu	Met	Gln	Ile	Arg	Pro	Ile	Val	Met
		340						345					350		
Ser	Gln	Lys	Asp	Gly	Asp	Arg	Pro	Lys	Lys	Lys	Val	Thr	Phe	Asn	Ser
		355					360					365			
Ser	Ser	Ile	Ile	Phe	Ile	Ile	Thr	Ser	Asp	Glu	Ser	Leu	Ser	Val	Asp
	370					375					380				
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Pro	Leu														

<210> 3

<211> 395
 <212> DNA
 <213> Homo sapien (human)

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 tgcatttgtg actggaactc ttctcgaaga ggctgccgct aaaccgcgtcc cacacgcagc 180
 ccacggtgtc ccacacccag ccgttcctca ggcaggacac gaaggtaaag gtgaccccgga 240
 agaggtacac agcagggtcgc tgaggctgat gttgaccagg aggaggtgag tgggagtgcg 300
 gagcgctgga acttgtagta gaggacgagc accagcaggt tgttgccgac gcccagcagc 360
 ccaatggagc ccagcagcag cgcaggccct cgtgc 395

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 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 4
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<210> 5
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

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<210> 6
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 6
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<210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 7

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22

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 8

gctgggcgctc ggcaacaa

18

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 9

caggcaggac acgaaggtaa

20

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 10

ggtcgctgag gctgatgttg ac

22

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 11

ggggatgtgc tgcaaggcga

20

<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 12

ccagggtttt cccagtcacg ac

22

<210> 13
 <211> 25
 <212> DNA
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<220>
 <223> Oligonucleotide

<400> 13
 cccaggcttt acactttatg cttcc

25

<210> 14
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 14
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25

<210> 15
 <211> 348
 <212> PRT
 <213> Homo sapien (human)

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 35 40 45
 Val Leu Gly Phe Pro Ile Asn Phe Leu Thr Leu Tyr Val Thr Val Gln
 50 55 60
 His Lys Lys Leu Arg Thr Pro Leu Asn Tyr Ile Leu Leu Asn Leu Ala
 65 70 75 80
 Val Ala Asp Leu Phe Met Val Leu Gly Gly Phe Thr Ser Thr Leu Tyr
 85 90 95
 Thr Ser Leu His Gly Tyr Phe Val Phe Gly Pro Thr Gly Cys Asn Leu
 100 105 110
 Glu Gly Phe Phe Ala Thr Leu Gly Gly Glu Ile Ala Leu Trp Ser Leu
 115 120 125
 Val Val Leu Ala Ile Glu Arg Tyr Val Val Val Cys Lys Pro Met Ser
 130 135 140
 Asn Phe Arg Phe Gly Glu Asn His Ala Ile Met Gly Val Ala Phe Thr
 145 150 155 160
 Trp Val Met Ala Leu Ala Cys Ala Ala Pro Pro Leu Ala Gly Trp Ser
 165 170 175
 Arg Tyr Ile Pro Glu Gly Leu Gln Cys Ser Cys Gly Ile Asp Tyr Tyr
 180 185 190

Thr	Leu	Lys	Pro	Glu	Val	Asn	Asn	Glu	Ser	Phe	Val	Ile	Tyr	Met	Phe	
		195					200					205				
Val	Val	His	Phe	Thr	Ile	Pro	Met	Ile	Ile	Ile	Phe	Phe	Cys	Tyr	Gly	
	210					215					220					
Gln	Leu	Val	Phe	Thr	Val	Lys	Glu	Ala	Ala	Ala	Gln	Gln	Gln	Glu	Ser	
225					230					235					240	
Ala	Thr	Thr	Gln	Lys	Ala	Glu	Lys	Glu	Val	Thr	Arg	Met	Val	Ile	Ile	
			245						250					255		
Met	Val	Ile	Ala	Phe	Leu	Ile	Cys	Trp	Val	Pro	Tyr	Ala	Ser	Val	Ala	
			260					265					270			
Phe	Tyr	Ile	Phe	Thr	His	Gln	Gly	Ser	Asn	Phe	Gly	Pro	Ile	Phe	Met	
	275						280					285				
Thr	Ile	Pro	Ala	Phe	Phe	Ala	Lys	Ser	Ala	Ala	Ile	Tyr	Asn	Pro	Val	
	290					295					300					
Ile	Tyr	Ile	Met	Met	Asn	Lys	Gln	Phe	Arg	Asn	Cys	Met	Leu	Thr	Thr	
305					310					315					320	
Ile	Cys	Cys	Gly	Lys	Asn	Pro	Leu	Gly	Asp	Asp	Glu	Ala	Ser	Ala	Thr	
			325						330					335		
Val	Ser	Lys	Thr	Glu	Thr	Ser	Gln	Val	Ala	Pro	Ala					
			340					345								